

Remote Use of Web 2.0 Technology by MSc Structural Molecular Biology Students from the Global South

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The School of Crystallography at Birkbeck College, London, has offered graduate courses in structural molecular biology by distance learning since 1996. Over 40 students have graduated with the full MSc in Structural Molecular Biology since that degree was introduced in 2001, and many others have obtained single Certificates after a year's part time study.

Our successful students have come from many countries and four continents, but until very recently almost all students from the global South have been excluded from the programme because of the relatively high fees. However, advanced training in the molecular biosciences is seen as a key to building independent research capacity and the potential for technology-led growth in these regions. We were awarded six Commonwealth Scholarships for the MSc course starting in October 2007, and by the time PCF5 is held these students will be close to completing the first double module of coursework, Principles of Protein Structure. We have incorporated material into this course that is specifically relevant to the development needs of these students' countries, and to the Millennium Development Goals relating to eradicating extreme poverty and combating infectious disease.

Structural biology is both a visual and a computationally-intensive subject, and students are expected to have access to sufficiently good computer and Internet resources to manipulate three-dimensional molecular images. The study experience can also be enriched by the use of Web 2.0 based "social software" and by software enabling student-tutor and student-student interactions in real time. Our Commonwealth Scholars are likely to be at a disadvantage when compared to other comparable students when using these tools, but the degree of this disadvantage will depend on the software used. We have been exploring the use of a number of different Web 2.0 based tools by all our distance learning students, including blogs, Wikis, shared bookmarking sites, real-time communication programs. In this presentation, I will describe the Commonwealth Scholars' experiences with these tools, how easy they find them to use with the hardware they have readily available and the extent to which these technologies help them to engage with the course material and their tutors and fellow students. I will also demonstrate the use of some of the tools.

INTRODUCTION

The School of Crystallography at Birkbeck College, London, has been in the forefront of Internet-based distance education at postgraduate level since the mid-1990s. The first Web-based certificate course, Principles of Protein Structure, was launched in 1996. Since 2001, we have offered a full Masters' degree. The MSc Structural Molecular Biology is a two-year, part-time modular course: all students take Principles of Protein Structure in the first year, and in the second they are offered a choice between a specialist module in protein crystallography and a more general one, Techniques in Structural Molecular Biology. That course includes the theory behind some basic molecular biology techniques, the three main structural biology techniques of X-ray crystallography, nuclear magnetic resonance and electron microscopy, and some biophysics including an introduction to protein-protein interactions. Bioinformatics, in the form of

computational analysis of protein sequences and structures, is covered where appropriate throughout the whole syllabus, and each course includes an element of independent project work. So far, about fifty students have obtained the MSc, and many others have passed one or more individual certificates. Some of these, taking the courses simply for continuing professional development, choose not to take examinations, so it is difficult to judge completion rates; however, since 2001 only six students who chose to take the full MSc have failed.

In the academic year 2008-9 the course structure will be changing to fit in with Birkbeck College's Common Awards scheme, with the whole course worth 180 credits at Master's level. Each taught double-module will be worth sixty credits, with the final sixty credits made up with project work. Exit points will be offered after sixty credits (for a Certificate) and 120 credits (for a Diploma).

Until very recently, the range of software that students use to display and interact with course material throughout the MSc programme of study has been relatively simple and straightforward. Teaching material is mounted on a dedicated web server, password protected and made available to registered students every few weeks, section by section. Principles of Protein Structure in particular, relies on the use of molecular visualization packages that allow students to manipulate molecules in three dimensions, to rotate, scale and alter display features in order to investigate aspects of their structure and function. We originally made extensive use of Rasmol (Sayle & Milner-White, 1995) which was perhaps the first affordable protein visualisation package that was fast enough to allow real-time image manipulation on desktop machines. We have now replaced this with Jmol, in which students can visualize interactive molecules embedded in web pages (Sansom *et al.*, 2005). Communication between students and teachers has generally been using email discussion lists and a text-based virtual reality environment, the "MUD" (Multi-User Dimension) which allows students and tutors to "chat" in real time. This technology flourished briefly in the 1990s and can be thought of as a precursor of the "social software" that is currently extremely popular. It is now relatively little used, but educationalists class it as a valid example of text-based real time communication that can offer "the ideal teaching situation of a tutor-student discussion, though at a distance" (Laurillard, 1993). In an early evaluation of the course technology (Sansom & Moss, 2000) the students described it as one of the most popular features of the course.

TEACHING STRUCTURAL BIOLOGY IN THE DEVELOPING WORLD

Distance learning in general is cost-effective when compared to similar programmes of study given face-to-face, particularly where the institution involved is located in as expensive a city as London. These courses can also be taken by students living at great distance from established centres of advanced scholarship. However, most potential students from developing and even middle-income countries are still unable to afford the fees charged even though, studying this type of course may be particularly important for students who are making their careers in such countries. In the late 1990s, the value of the course to students in eastern and central Europe – then barely recovering from decades of neglect during the Cold War – was recognized with grants from the Open Society Institute that enabled forty students from former Communist countries to take the Principles of Protein Structure course.

There is also a clear link between the academic discipline of structural molecular biology and the Millennium Development Goals. Solving the molecular structures of proteins from human and animal pathogens endemic in developing countries is an important step in understanding the processes of infection and developing successful drugs and vaccines against the diseases they cause. This builds on genomic science, with the complete genome sequences of many such pathogens available in the public domain. For example, significant structural biology resources have been focused on *Mycobacterium tuberculosis*, the causative agent of tuberculosis which still

kills well over a million people each year (Arcus *et al.*, 2006); efforts are under way to design inhibitors to *M. tuberculosis* proteins that are functional in the latent or the active phases of TB infection. Nicholas Keep and co-workers at Birkbeck College recently determined the structure of a key *M. tuberculosis* protein that is known to be involved in promoting the activation of dormant *Mycobacteria* (Cohen-Gonsaud *et al.*, 2005).

The importance of keeping the ownership and control of science related to Third World priorities in the hands of Third World scientists has now been recognized, and, where such subjects have historically been severely under-funded, distance learning programs can go a long way to providing the training needs of key personnel. Recognising this, we have sought funding to enable students from developing countries who could not otherwise afford the course fees to participate. Last year, we were successful in obtaining an award from the Commonwealth Scholarship Commission of the Association of Commonwealth Universities to enable six students from developing Commonwealth countries to commence the MSc programme in 2007; we were awarded eight scholarships from the same source for students to begin in October 2008. The first tranche of Commonwealth Scholars includes one student from each of the Cameroon, Bangladesh, India and Guyana, and two from Kenya. We are extending our course material to cover topics of particular importance in the home countries of our current and potential Commonwealth Scholars, including microbial genome projects, structures of protein drug targets from HIV and influenza, and vaccine design. Our collaborator Richard Bishop of the International Livestock Research Institute, Nairobi, Kenya and his co-workers have sequenced the genome of the protozoal pathogen *Theileria parva*, the causative agent of East Coast fever in cattle (Gardner *et al.*, 2005) and are using the sequence to develop potential vaccines against this endemic livestock disease.

WEB 2.0 BASED SOCIAL SOFTWARE

All students of web-based courses hosted by the School of Crystallography are expected to have regular access to reasonably fast Internet connection and to computer hardware that is powerful enough to allow them to manipulate molecular structures in “real time”. Students are also expected to be able to contribute actively to online discussions with tutors and their peers. Although Internet access is growing throughout the world, and Africa had the second highest percentage growth in users of any world region between 2000 and 2007 (<http://www.internetworldstats.com/stats.htm>), Commonwealth Scholars and other students from poorer countries can still be expected to be at a disadvantage. Since the launch of the first course, we have maintained the rule that all software used for compulsory parts of our courses must be usable on all widely used operating systems (Windows, Mac OS and Unix); must run on relatively old machines; and must be usable over slow internet connections. It is important to remember that dialup is still the most common way of connecting to the Internet in many Third World countries, particularly in sub-Saharan Africa.

The text-based programs that, until 2007, we relied on for communication between students and tutors – email discussion lists and the “MUD” environment for interactive tutorials – fulfill these criteria very adequately. However, we were spurred to evaluate a range of Web 2.0 based “social software” programs at least partly by a perception that the MUDs, in particular, were becoming less popular with our students, just as blogs, wikis and social networking sites were becoming almost ubiquitous. As early as 2004, a US-based biochemistry lecturer commented that “Many of our students are consummate bloggers who are attuned to a cyber feed of constant information ... I must appreciate [this technology] to stay in touch with the milieu of my students” (Parslow, 2004). Higher education cannot afford to offer students technology that is significantly inferior to that they interact with regularly in their everyday lives. We are seeking to establish the extent to which social software enables students to engage more closely with the course material, tutors and their peers. One of our most important priorities is to establish whether these tools are, in fact,

equally accessible to all students, including students in industry and disabled students as well as those disadvantaged by slow Internet connections and low performance machines.

STUDY METHODOLOGY

In December 2007, two months after the start of the MSc, we surveyed all thirty registered students on the Principles of Protein Structure course for their experience with, and opinions of, the software used in the course as well as the programs to be piloted. We asked students how often they interacted with the course in different ways (reading material online, responding to posts on the discussion list, using molecular visualization software, attending tutorial sessions in the "MUD", etc.); how useful they found each of these; how they rated the MUD discussions in particular; and what experience they had of using blogs, wikis and other types of social software outside the course.

Since then, we have been introducing social software products into the Principles of Protein Structure course and monitoring how it is used. We are evaluating these throughout the year using a set of criteria that will determine how each is used in future years. High priority will be given to tools that can be used with low specification technology and through dialup connections, which are likely to be particularly valued by students from the global South. Therefore, the "immersive virtual environment" Second Life, which requires high specification hardware and a very fast, reliable Internet connection, is being investigated only as a potential "optional extra" for some of our students. Although it is being increasingly used in higher education in the UK (Kirriemuir, 2007) many educationalists are concerned about these requirements and it has been described as "a luxury" (Peter Murray-Rust, personal communication). This technology cannot be considered relevant to the needs of the developing world and it will not be further considered here.

We have established a blog for the course (<http://principlesofproteinstructure.blogspot.com>). This is "open" for all students to comment on entries, and students have also been invited to register and make posts. This aims to link current research presented at conferences and seminars with the course content more directly than is possible in the (mainly) static course material. The regular tutorials using the original MUD software are now being supplemented with similar sessions using Instant Messenger software, trying out tools from different providers including AOL and Microsoft Messenger, which are probably the most widely used. We have encouraged students to store, tag and share their favourite databases and websites in the area of protein structure research using the social bookmarking tool del.icio.us (<http://del.icio.us/about>).

The course includes a dissertation on an aspect of protein structure, which the students work on during the summer for submission in October, a month after the examination. These are written in HTML and mounted from the course website, and a small percentage of the marks are awarded for style and Web presentation skills. This year, we will also be asking students, as part of their dissertation work, to contribute terms and definitions in the research areas they are studying to a wiki which will later form a resource for future students that can be added to in subsequent years.

INITIAL OUTCOMES AND CONCLUSIONS

Out of thirty students registered on the Principles of Protein Structure course in December 2007, twenty-seven (90%) completed at least some of the questionnaire and twenty-one (70%) answered all questions; this is an extremely high response rate. The 27 respondents included four of the six Commonwealth Scholars, from Africa and South Asia. These four students have

been among the more “interactive” students in the course overall; the other two (from Guyana and Kenya) have reported more general problems with accessing the course material. However, all Scholars are making at least satisfactory overall progress, with the average score for the six students in the first assignment very close to that for the cohort as a whole.

The “snapshot” of Web 2.0 based software use obtained by the questionnaire indicated that the most widely used tools were Instant Messenger and the very popular “social networking” sites such as Facebook and MySpace (which are generally regarded to be of very limited use in education). Interestingly, few were using wikis regularly, and even fewer, blogs (although it is not clear whether students regarded merely viewing a blog as “using” it) and few had heard of Second Life. In general, the four Commonwealth Scholars were slightly, but not significantly, less familiar with this software than their peers in other countries. In contrast, however, they valued the MUD – at the time, the only method used for “real time” communication with students – rather more highly than the “average” student.

It is still rather early to judge the extent to which all students are engaging with, and benefiting from, the new tools being introduced during the course. It is clear, however, that all students, even those using dialup, are finding Instant Messenger faster than the original MUD software, and that it is generally easier to follow threads in the discussion; there are, however, problems with joining sessions and with server reliability. The blog is widely viewed, but it is, not unexpectedly, proving harder to persuade students to make posts. By the time of the conference, the students will have more experience of these tools and will be beginning to use a wiki for their dissertations. I will describe the experience of a representative group of students, including Commonwealth Scholars, and report on the extent to which the software has helped all students, but particularly those from the global South, become part of the learning community at Birkbeck and engage fully with this complex and important area of modern molecular biology.

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